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Reporting Summary

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in the figure regent, that the following items are present in the figure regent, table regent, main text, or interious section.
n/a Confirmed
The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
The statistical test(s) used AND whether they are one- or two-sided Only common tests should be described solely by name; describe more complex techniques in the Methods section.
A description of all covariates tested
A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted Give <i>P</i> values as exact values whenever suitable.
For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), indicating how they were calculated
Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.
Software and code

Policy information about availability of computer code

Data collection Fluorescent data from microplate were collected with Gen5 2.07 (Biotek). Bacterial colony counts were obtained by serial dilutions and plating

on LB agar plates.

Data analysis

Graphs were plotted with and appropriate statistical analyses were conducted using GraphPad Prism version 6 (*p < 0.05, **p < 0.01, ***p < 0.01, **p < 0.01 0.001, ****p < 0.0001).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and $reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research <math display="block"> \underbrace{\text{guidelines for submitting code \& software}}_{\text{code & work of the Nature}} \text{ for further information}.$

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The authors declare that the data supporting the findings of this study are

available within the paper and its supplementary information files. Source data are provided with this paper.

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Please select the o	ne below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.
X Life sciences	Behavioural & social sciences Ecological, evolutionary & environmental sciences
For a reference copy of	the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf
Life scier	nces study design
All studies must dis	sclose on these points even when the disclosure is negative.
Sample size	For in vitro experiments, sample size of $n = 3 - 6$ was used as a conservative approach based on estimations of effect size from preliminary experiments to reach a statistical power equal to or greater than 0.8
Data exclusions	Data was not excluded from analysis.
Replication	Experiments in Fig. 1B, C; Fig. 2B, C; Fig. 3B, Fig. 4, and Fig. 5, were reproduced 3 times total with similar results. Experiments in Fig. 2E, Fig. 3C, D, E; and Fig. 7B were reproduced 2 times total with similar results. Experiments in Fig. 2D and 7A were performed once.
Randomization	All biological species (i.e., bacteria) were randomly pulled from a well-mixed solution. No animal experiments were performed in this study.
Blinding	All samples were placed in wells according to group and notated in lab notebook. These labels were hidden during the collection of data for the experiment, and were not revealed until after data was collected. These labels were input into GraphPad software for plot creation, at which point the labels were known. However, the statistical analysis was automated by GraphPad so at this point the labels were blinded.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems			Methods		
n/a	Involved in the study	n/a	Involved in the study		
x	Antibodies	×	ChIP-seq		
X	☐ Eukaryotic cell lines	X	Flow cytometry		
×	Palaeontology and archaeology	×	MRI-based neuroimaging		
×	Animals and other organisms				
	🗶 Human research participants				
×	Clinical data				
×	Dual use research of concern				

Human research participants

Policy information about studies involving human research participants

Population characteristics

There was no population involved with the study - blood was obtained from a single donor.

Recruitment

Participants were recruited on a volunteer basis - primary selection criteria were that the blood donors were considered healthy and had abstained from using aspirin in the last two weeks.

Ethics oversight

Written informed consent was obtained according to protocol approved by Georgia Tech Institutional Review Board: GT IRB H15258.

Note that full information on the approval of the study protocol must also be provided in the manuscript.